

PC-0052 CIP

<110> Xu, Hong
Cohan, Victoria L.
Stuart, Susan G.

<120> HUMAN EMR1-LIKE G PROTEIN-COUPLED RECEPTOR

<130> PC-0052 CIP

<140> To Be Assigned

<141> Herewith

<160> 12

<170> PERL Program

<210> 1

<211> 652

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 429905

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Pro	Leu	Glu	Thr	Cys	Asn	Asp	Ile	Asn	Glu	Cys	Thr	Pro	Pro	Tyr
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Ser	Val	Tyr	Cys	Gly	Phe	Asn	Ala	Val	Cys	Tyr	Asn	Val	Glu	Gly
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Val	Asp	Lys	Phe	Glu	Ser	Leu	Leu	Thr	Asn	Gln	Thr	Leu	Trp	Arg
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Thr	Glu	Gly	Arg	Gln	Glu	Ile	Ser	Ser	Thr	Ala	Thr	Thr	Ile	Leu
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Arg	Asp	Val	Glu	Ser	Lys	Val	Leu	Glu	Thr	Ala	Leu	Lys	Asp	Pro
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Thr	Gln	Ala	Ile	Thr	Asp	Asn	Cys	Ser	Glu	Glu	Arg	Lys	Thr	Phe
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Asn	Leu	Asn	Val	Gln	Met	Asn	Ser	Met	Asp	Ile	Arg	Cys	Ser	Asp
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Ser	Ala	Ala	Ile	Gly	Pro	Lys	Arg	Asn	Val	Ser	Leu	Ser	Lys	Ser
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Lys	Val	Phe	Cys	Val	Tyr	Trp	Lys	Ser	Thr	Gly	Gln	Gly	Ser	Gln
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Ile	Val	Lys	Ser	Lys	Ser	Glu	Ser	Glu	Thr	Tyr	Thr	Leu	Ser	Ser	
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Lys	Met	Gly	Pro	Asp	Ser	Lys	Pro	Ser	Glu	Gly	Asp	Val	Phe	Pro	
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 <223> Incyte ID No: 429905

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 <222> 3293
 <223> a, t, c, g, or other

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<212> DNA
<213> Homo sapiens

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<221> unsure
<222> 4, 8, 16, 19, 65
<223> a, t, c, g, or other

<400> 3

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<211> 320

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 1837630F6

<400> 4

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gaaaaccaa acttcctgtg ctaagtgcgc cccaaatgct tcctgtgtca ataactca 180
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<211> 624

<212> DNA

<213> Homo sapiens

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<210> 7

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<213> Homo sapiens

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tgtgagtgtc gctatggacc caaaaggaac gtgtctctct ccaagtctgt gacgctgact 180
ttccagcacg tgaagatgac ccccgatgcc aaaaaggctc tctgtgtcta ctggaagagc 240
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acaccatgtg taattgcagt cacctgtcca gcttcgctgt cctgatggcc ctgaccagcc 360
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<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 320551R1

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<222> 6, 17, 76, 105

<223> a, t, c, g, or other

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gaaaatatta aaactaggaa tattcaactc catatggaaa atcatatcca tggatctctt 300
tggcattatg aagaatgaag ctaaggaaaa gggaattcat taaacatatc atccttgag 360
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atgaactcaa tggacatccg ttgcagtgc atcatccagg gagacacaca aggtcccagt 240
gccattgcct ttatctcata ttcttctctt ggaaacatca taaatgcaac tttttttgaa 300
gagatggata agaaagatca agtgtatctg aactctcagg ttgtgagtgc tgctattgga 360
cccaaaagga acgtgtctct ctccaagtct gtgacgctga ctttccagca cgtgaagat 419
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<210> 10

<211> 598

<212> DNA

<213> Homo sapiens

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<210> 11

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<212> PRT

<213> Homo sapiens

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<308> Genbank ID No: g784994

<400> 11

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35 40 45
Thr Cys Thr Asn Thr Val Asp Ser Tyr Tyr Cys Thr Cys Lys Gln
50 55 60
Gly Phe Leu Ser Ser Asn Gly Gln Asn His Phe Lys Asp Pro Gly
65 70 75
Val Arg Cys Lys Asp Ile Asp Glu Cys Ser Gln Ser Pro Gln Pro
80 85 90
Cys Gly Pro Asn Ser Ser Cys Lys Asn Leu Ser Gly Arg Tyr Lys
95 100 105
Cys Ser Cys Leu Asp Gly Phe Ser Ser Pro Thr Gly Asn Asp Trp
110 115 120
Val Pro Gly Lys Pro Gly Asn Phe Ser Cys Thr Asp Ile Asn Glu
125 130 135
Cys Leu Thr Ser Arg Val Cys Pro Glu His Ser Asp Cys Val Asn
140 145 150
Ser Met Gly Ser Tyr Ser Cys Ser Cys Gln Val Gly Phe Ile Ser
155 160 165
Arg Asn Ser Thr Cys Glu Asp Val Asn Glu Cys Ala Asp Pro Arg
170 175 180
Ala Cys Pro Glu His Ala Thr Cys Asn Asn Thr Val Gly Asn Tyr
185 190 195
Ser Cys Phe Cys Asn Pro Gly Phe Glu Ser Ser Ser Gly His Leu
200 205 210
Ser Cys Gln Gly Leu Lys Ala Ser Cys Glu Asp Ile Asp Glu Cys
215 220 225
Thr Glu Met Cys Pro Ile Asn Ser Thr Cys Thr Asn Thr Pro Gly
230 235 240
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245 250 255
Gln Leu Asn Phe Thr Asp Gln Gly Val Glu Cys Arg Asp Ile Asp
260 265 270
Glu Cys Arg Gln Asp Pro Ser Thr Cys Gly Pro Asn Ser Ile Cys
275 280 285
Thr Asn Ala Leu Gly Ser Tyr Ser Cys Gly Cys Ile Val Gly Phe
290 295 300
His Pro Asn Pro Glu Gly Ser Gln Lys Asp Gly Asn Phe Ser Cys
305 310 315
Gln Arg Val Leu Phe Lys Cys Lys Glu Asp Val Ile Pro Asp Asn
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Lys Gln Ile Gln Gln Cys Gln Glu Gly Thr Ala Val Lys Pro Ala
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				365					370					375
Thr	Thr	Glu	Ser	Phe	Val	Pro	Val	Leu	Lys	Gln	Ile	Ser	Met	Trp
				380					385					390
Thr	Lys	Phe	Thr	Lys	Glu	Glu	Thr	Ser	Ser	Leu	Ala	Thr	Val	Phe
				395					400					405
Leu	Glu	Ser	Val	Glu	Ser	Met	Thr	Leu	Ala	Ser	Phe	Trp	Lys	Pro
				410					415					420
Ser	Ala	Asn	Val	Thr	Pro	Ala	Val	Arg	Ala	Glu	Tyr	Leu	Asp	Ile
				425					430					435
Glu	Ser	Lys	Val	Ile	Asn	Lys	Glu	Cys	Ser	Glu	Glu	Asn	Val	Thr
				440					445					450
Leu	Asp	Leu	Val	Ala	Lys	Gly	Asp	Lys	Met	Lys	Ile	Gly	Cys	Ser
				455					460					465
Thr	Ile	Glu	Glu	Ser	Glu	Ser	Thr	Glu	Thr	Thr	Gly	Val	Ala	Phe
				470					475					480
Val	Ser	Phe	Val	Gly	Met	Glu	Ser	Val	Leu	Asn	Glu	Arg	Phe	Phe
				485					490					495
Gln	Asp	His	Gln	Ala	Pro	Leu	Thr	Thr	Ser	Glu	Ile	Lys	Leu	Lys
				500					505					510
Met	Asn	Ser	Arg	Val	Val	Gly	Gly	Ile	Met	Thr	Gly	Glu	Lys	Lys
				515					520					525
Asp	Gly	Phe	Ser	Asp	Pro	Ile	Ile	Tyr	Thr	Leu	Glu	Asn	Val	Gln
				530					535					540
Pro	Lys	Gln	Lys	Phe	Glu	Arg	Pro	Ile	Cys	Val	Ser	Trp	Ser	Thr
				545					550					555
Asp	Val	Lys	Gly	Gly	Arg	Trp	Thr	Ser	Phe	Gly	Cys	Val	Ile	Leu
				560					565					570
Glu	Ala	Ser	Glu	Thr	Tyr	Thr	Ile	Cys	Ser	Cys	Asn	Gln	Met	Ala
				575					580					585
Asn	Leu	Ala	Val	Ile	Met	Ala	Ser	Gly	Glu	Leu	Thr	Met	Asp	Phe
				590					595					600
Ser	Leu	Tyr	Ile	Ile	Ser	His	Val	Gly	Ile	Ile	Ile	Ser	Leu	Val
				605					610					615
Cys	Leu	Val	Leu	Ala	Ile	Ala	Thr	Phe	Leu	Leu	Cys	Arg	Ser	Ile
				620					625					630
Arg	Asn	His	Asn	Thr	Tyr	Leu	His	Leu	His	Leu	Cys	Val	Cys	Leu
				635					640					645
Leu	Leu	Ala	Lys	Thr	Leu	Phe	Leu	Ala	Gly	Ile	His	Lys	Thr	Asp
				650					655					660
Asn	Lys	Thr	Gly	Cys	Ala	Ile	Ile	Ala	Gly	Phe	Leu	His	Tyr	Leu
				665					670					675
Phe	Leu	Ala	Cys	Phe	Phe	Trp	Met	Leu	Val	Glu	Ala	Val	Ile	Leu
				680					685					690
Phe	Leu	Met	Val	Arg	Asn	Leu	Lys	Val	Val	Asn	Tyr	Phe	Ser	Ser
				695					700					705
Arg	Asn	Ile	Lys	Met	Leu	His	Ile	Cys	Ala	Phe	Gly	Tyr	Gly	Leu
				710					715					720
Pro	Met	Leu	Val	Val	Val	Ile	Ser	Ala	Ser	Val	Gln	Pro	Gln	Gly
				725					730					735
Tyr	Gly	Met	His	Asn	Arg	Cys	Trp	Leu	Asn	Thr	Glu	Thr	Gly	Phe
				740					745					750
Ile	Trp	Ser	Phe	Leu	Gly	Pro	Val	Cys	Thr	Val	Ile	Val	Ile	Asn
				755					760					765
Ser	Leu	Leu	Leu	Thr	Trp	Thr	Leu	Trp	Ile	Leu	Arg	Gln	Arg	Leu
				770					775					780
Ser	Ser	Val	Asn	Ala	Glu	Val	Ser	Thr	Leu	Lys	Asp	Thr	Arg	Leu
				785					790					795
Leu	Thr	Phe	Lys	Ala	Phe	Ala	Gln	Leu	Phe	Ile	Leu	Gly	Cys	Ser
				800					805					810
Trp	Val	Leu	Gly	Ile	Phe	Gln	Ile	Gly	Pro	Val	Ala	Gly	Val	Met
				815					820					825
Ala	Tyr	Leu	Phe	Thr	Ile	Ile	Asn	Ser	Leu	Gln	Gly	Ala	Phe	Ile
				830					835					840
Phe	Leu	Ile	His	Cys	Leu	Leu	Asn	Gly	Gln	Val	Arg	Glu	Glu	Tyr

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				845					850				855	
Lys	Arg	Trp	Ile	Thr	Gly	Lys	Thr	Lys	Pro	Ser	Ser	Gln	Ser	Gln
				860					865					870
Thr	Ser	Arg	Ile	Leu	Leu	Ser	Ser	Met	Pro	Ser	Ala	Ser	Lys	Thr
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Gly														

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His	Trp	Ala	Thr	Thr	Gly	Cys	Ser	Thr	Ile	Gly	Thr	Arg	Asp	Thr
				20					25					30
Ser	Thr	Ile	Cys	Arg	Cys	Thr	His	Leu	Ser	Ser	Phe	Ala	Val	Leu
				35					40					45
Met	Ala	His	Tyr	Asp	Val	Gln	Glu	Asp	Pro	Val	Leu	Thr	Val	Ile
				50					55					60
Thr	Tyr	Met	Gly	Leu	Ser	Val	Ser	Leu	Leu	Cys	Leu	Leu	Leu	Ala
				65					70					75
Ala	Leu	Thr	Phe	Leu	Leu	Cys	Lys	Ala	Ile	Gln	Asn	Thr	Ser	Thr
				80					85					90
Ser	Leu	His	Leu	Gln	Leu	Ser	Leu	Cys	Leu	Phe	Leu	Ala	His	Leu
				95					100					105
Leu	Phe	Leu	Val	Ala	Ile	Asp	Gln	Thr	Gly	His	Lys	Val	Leu	Cys
				110					115					120
Ser	Ile	Ile	Ala	Gly	Thr	Leu	His	Tyr	Leu	Tyr	Leu	Ala	Thr	Phe
				125					130					135
Thr	Trp	Met	Leu	Leu	Glu	Ala	Leu	Tyr	Leu	Phe	Leu	Thr	Ala	Arg
				140					145					150
Asn	Leu	Thr	Val	Val	Asn	Tyr	Ser	Ser	Ile	Asn	Arg	Phe	Met	Lys
				155					160					165
Lys	Leu	Met	Phe	Pro	Val	Gly	Tyr	Gly	Val	Pro	Ala	Val	Thr	Val
				170					175					180
Ala	Ile	Ser	Ala	Ala	Ser	Arg	Pro	His	Leu	Tyr	Gly	Thr	Pro	Ser
				185					190					195
Arg	Cys	Trp	Leu	Gln	Pro	Glu	Lys	Gly	Phe	Ile	Trp	Gly	Phe	Leu
				200					205					210
Gly	Pro	Val	Cys	Ala	Ile	Phe	Ser	Val	Asn	Leu	Val	Leu	Phe	Leu
				215					220					225
Val	Thr	Leu	Trp	Ile	Leu	Lys	Asn	Arg	Leu	Ser	Ser	Leu	Asn	Ser
				230					235					240
Glu	Val	Ser	Thr	Leu	Arg	Asn	Thr	Arg	Met	Leu	Ala	Phe	Lys	Ala
				245					250					255
Thr	Ala	Gln	Leu	Phe	Ile	Leu	Gly	Cys	Thr	Trp	Cys	Leu	Gly	Ile
				260					265					270
Leu	Gln	Val	Gly	Pro	Ala	Ala	Arg	Val	Met	Ala	Tyr	Leu	Phe	Thr
				275					280					285
Ile	Ile	Asn	Ser	Leu	Gln	Gly	Val	Phe	Ile	Phe	Leu	Val	Tyr	Cys
				290					295					300
Leu	Leu	Ser	Gln	Gln	Val	Arg	Glu	Gln	Tyr	Gly	Lys	Trp	Ser	Lys
				305					310					315
Gly	Ile	Arg	Lys	Leu	Lys	Thr	Glu	Ser	Glu	Met	His	Thr	Leu	Ser
				320					325					330
Ser	Ser	Ala	Lys	Ala	Asp	Thr	Ser	Lys	Pro	Ser	Thr	Val	Asn	
				335					340					